



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 [Filter](#) ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black




☐ Show CDS translation [Align](#)

Sequence 1: unnamed protein product - *human soluble epoxide hydrolase*
Length = 556

Sequence 2: unnamed protein product - *human renin*
Length = 406

No significant similarity was found

CPU time: 0.03 user secs. 0.02 sys. secs 0.05 total secs.

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Range: from begin to end Features: ☒ CDD

☐ 1: [AAG14968](#). Reports soluble epoxide h...[gi:10197684]

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LOCUS AAG14968 556 aa linear PRI 20-SEP-2000
 DEFINITION soluble epoxide hydrolase [Homo sapiens].
 ACCESSION AAG14968
 VERSION AAG14968.1 GI:10197684
 DBSOURCE locus AF233336 accession [AF233336.1](#)
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 556)
 AUTHORS Sandberg,M., Hassett,C., Adman,E.T., Meijer,J. and Omiecinski,C.J.
 TITLE Identification and functional characterization of human soluble
 epoxide hydrolase genetic polymorphisms
 JOURNAL J. Biol. Chem. 275 (37), 28873-28881 (2000)
 PUBMED [10862610](#)
 REFERENCE 2 (residues 1 to 556)
 AUTHORS Hassett,C.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2000) Environmental Health, University of
 Washington, 4225 Roosevelt Way NE #100, Seattle, WA 98105, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..556
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8p21-p12"
 /clone="129-13"
 /sex="female"
 /tissue_type="liver"
 Protein 1..556
 /product="soluble epoxide hydrolase"
 /EC_number="3.3.2.3"
 Region 1..212
 /region_name="COG1011"
 /note="Predicted hydrolase (HAD superfamily) [General
 function prediction only]; COG1011"
 /db_xref="CDD:31215"
 Region 234..545
 /region_name="PldB"
 /note="Lysophospholipase [Lipid metabolism]; COG2267"
 /db_xref="CDD:32448"
 Region 286..541

CDS

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/region_name="Abhydrolase_1"  
/note="alpha/beta hydrolase fold. This catalytic domain is  
found in a very wide range of enzymes; pfam00561"  
/db_xref="CDD:84863"  
1..556  
/gene="EPHX2"  
/coded_by="AF233336.1:35..1705"  
/note="putative mutant sEH"
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ORIGIN

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1 mtlraavfdl dgvlalpavf gvlgrteeal alprgllnda fqkggpegat trlmkgeitl  
61 sqwiplmeen crkcsetakv clpknfsike ifdkaisark inrpmlqaal mlrkkgftta  
121 iltntwladdr aerdglaqlm celkmhfdfl iescqvgmvk pepqiykfl1 dtlkaspsev  
181 vflddiganl kpardlgmvt ilvqdttdal kelekvtgiq llntpaplpt scnpsdmsgh  
241 yvtvkprvrl hfvelgsgpa vclchgfpes wyswryqipa laqagyrvla mdmkgygess  
301 appeieeycm evlckemvtf ldklglsqav fighdwggml vwymalfype rvravaslnt  
361 pfipanpnms plesikanpv fdyqlyfqep gvaeeleqn lsrrtfkslf rasdesvlsm  
421 hkvceaggfl vnspeeps1s rmvteeeiqf yvqqfkkskf rgplnwyrnm ernwkwacks  
481 lgrkilipal mvtaekdfvl vpqmsqhmed wiph1krghi edcghwtqmd kptevnqili  
541 kwldsdarnp pvvskm
```

//

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Range: from begin to end Features: ☒ CDD

☐ 1: AAA60363. Reports renin [Homo sapie...[gi:190994]

BLink. Conserved Domains, Links

Features Sequence

LOCUS AAA60363 406 aa linear PRI 21-OCT-2002
 DEFINITION renin [Homo sapiens].
 ACCESSION AAA60363
 VERSION AAA60363.1 GI:190994
 DBSOURCE locus HUMREN01 accession [L00064.1](#)
 locus HUMREN02 accession [L00065.1](#)
 locus HUMREN03 accession [L00066.1](#)
 locus HUMREN04 accession [L00067.1](#)
 locus HUMREN05 accession [L00068.1](#)
 locus HUMREN06 accession [L00069.1](#)
 locus HUMREN07 accession [L00070.1](#)
 locus HUMREN08 accession [L00071.1](#)
 locus HUMREN09 accession [L00072.1](#)
 locus HUMREN10 accession [L00073.1](#)
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 406)
 AUTHORS Miyazaki,H., Fukamizu,A., Hirose,S., Hayashi,T., Hori,H.,
 Ohkubo,H., Nakanishi,S. and Murakami,K.
 TITLE Structure of the human renin gene
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (19), 5999-6003 (1984)
 PUBMED [6091130](#)
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /map="lq32"
 /dev_stage="foetus"
 /tissue_lib="T.Maniatis"
 Protein 1..406
 /product="renin"
 sig_peptide 1..33
 mat_peptide 67..406
 /product="renin"
 CDS 1..406
 /gene="REN"
 /coded_by="join(L00064.1:593..690,L00065.1:127..277,
 L00066.1:24..147,L00067.1:14..132,L00068.1:24..220,
 L00069.1:29..37,L00070.1:55..174,L00071.1:13..154,
 L00072.1:34..132,L00073.1:71..232)"

/note="precursor"

ORIGIN

```
1 mdgwrrmprw gllllllwgsc tfglptdttt fkriflkrmp sireslkerg vdmarglpew
61 sqpmkrltlg nttssvilt n ymdtqyygei gigtppqtfk vvf dtgssnv wvpsskcsrl
121 ytacvyhklf dasdsssykh ng tel tlr ys t gtvsgflsq diitv ggitv tqmfgevt em
181 palpfmlaef dgvvvgmgfie qaigrvtpif dniisqgvk edv fsfyynr dsensqslgg
241 qivlggsdpq hyegnfhyin liktgvwqi q mkgvsvgsst llcedgclal vdtgasyisg
301 stssieklme algakkrlfd yvvkcnegpt lpdisfhlgg keytltsady vfqesysskk
361 lctlaihamd ippptgptwa lgatfirkfy tefdrnnri gfalar
```

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